

2848-56-PCT.ST25.txt
SEQUENCE LISTING

<110> Hutton, John C.
O'Brien, Richard
Davidson, Howard
Hackl, Seija

<120> Use of Islet Glucose-6-Phosphatase Related Protein as a
Diagnostic Tool and Therapeutic Target for Autoimmune Diabetes

<130> 2848-56-PCT

<150> US 60/505317

<151> 2003-09-22

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 1068

<212> DNA

<213> Homo sapiens

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<221> CDS

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aag gac tac cga gct tac tac act ttt cta aat ttt atg tcc aat gtt

96

Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val
20 25 30

gga gac ccc agg aat atc ttt ttc att tat ttt cca ctt tgt ttt caa

144

Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln
35 40 45

ttt aat cag aca gtt gga acc aag atg ata tgg gta gca gtc att ggg

192

Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
50 55 60

gat tgg tta aat ctt ata ttt aaa tgg ata tta ttt ggt cat cga cct

240

Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
65 70 75 80

tac tgg tgg gtc caa gaa act cag att tac cca aat cac tca agt cca

288

Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro
85 90 95

tgc ctt gaa cag ttc cct act aca tgt gaa aca ggt cca gga agt cca

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336
 Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
 100 105 110
 tct ggc cat gca atg ggc gca tcc tgt gtc tgg tat gtc atg gta acc
 384
 Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr
 115 120 125
 gct gcc ctg agc cac act gtc tgt ggg atg gat aag ttc tct atc act
 432
 Ala Ala Leu Ser His Thr Val Cys Gly Met Asp Lys Phe Ser Ile Thr
 130 135 140
 ctg cac aga ctg acc tgg tca ttt ctt tgg agt gtt ttt tgg ttg att
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 Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
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 528
 Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
 165 170 175
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 576
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 180 185 190
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 624
 Phe Glu His Thr Pro Gly Ile Gln Thr Ala Ser Leu Gly Thr Tyr Leu
 195 200 205
 aag acc aac ctc ttt ctc ttc ctg ttt gca gtt ggc ttt tac ctg ctt
 672
 Lys Thr Asn Leu Phe Leu Phe Leu Phe Ala Val Gly Phe Tyr Leu Leu
 210 215 220
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 720
 Leu Arg Val Leu Asn Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
 225 230 235 240
 aag tgg tgt gct aac ccc gac tgg atc cac att gac acc acg cct ttt
 768
 Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Thr Thr Pro Phe
 245 250 255
 gct gga ctc gtg aga aac ctt ggg gtc ctc ttt ggc ttg ggc ttt gca
 816
 Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala
 260 265 270
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 864

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Ile Asn Ser Glu Met Phe Leu Leu Ser Cys Arg Gly Gly Asn Asn Tyr
 275 280 285

aca ctg agc ttc cgg ttg ctc tgt gcc ttg acc tca ttg aca ata ctg

912
 Thr Leu Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Ile Leu
 290 295 300

cag ctc tac cat ttc ctc cag atc ccg act cac gaa gag cat tta ttt

960
 Gln Leu Tyr His Phe Leu Gln Ile Pro Thr His Glu Glu His Leu Phe
 305 310 315 320

tat gtg ctg tct ttt tgt aaa agt gca tcc att ccc cta act gtg gtt

1008
 Tyr Val Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Thr Val Val
 325 330 335

gct ttc att ccc tac tct gtt cat atg tta atg aaa caa agc gga aag

1056
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1068
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 <213> Homo sapiens

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Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val
 20 25 30

Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln
 35 40 45

Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
 50 55 60

Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
 65 70 75 80

Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro
 85 90 95

Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
 100 105 110

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Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr
 115 120
 Ala Ala Leu Ser His Thr Val Cys Gly Met Asp Lys Phe Ser Ile Thr
 130 135 140
 Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
 145 150 155 160
 Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
 165 170 175
 His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
 180 185
 Phe Glu His Thr Pro Gly Ile Gln Thr Ala Ser Leu Gly Thr Tyr Leu
 195 200 205
 Lys Thr Asn Leu Phe Leu Phe Leu Phe Ala Val Gly Phe Tyr Leu Leu
 210 215 220
 Leu Arg Val Leu Asn Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
 225 230 235 240
 Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Thr Thr Pro Phe
 245 250 255
 Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala
 260 265 270
 Ile Asn Ser Glu Met Phe Leu Leu Ser Cys Arg Gly Gly Asn Asn Tyr
 275 280 285
 Thr Leu Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Ile Leu
 290 295 300
 Gln Leu Tyr His Phe Leu Gln Ile Pro Thr His Glu Glu His Leu Phe
 305 310 315 320
 Tyr Val Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Thr Val Val
 325 330 335
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<222> (63)..(1127)

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107

Met Asp Phe Leu His Arg Ser Gly Val Leu Ile Ile His His Leu
1 5 10 15

cag gag gac tac cgg act tac tat ggt ttt cta aat ttt atg tcc aat

155

Gln Glu Asp Tyr Arg Thr Tyr Tyr Gly Phe Leu Asn Phe Met Ser Asn
20 25 30

gtt gga gac ccc cga aat atc ttt tct att tac ttc cca ctt tgg ttt

203

Val Gly Asp Pro Arg Asn Ile Phe Ser Ile Tyr Phe Pro Leu Trp Phe
35 40 45

cag ttg aat cag aat gtt gga acc aag atg atc tgg gta gcg gtc ata

251

Gln Leu Asn Gln Asn Val Gly Thr Lys Met Ile Trp Val Ala Val Ile
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ggg gac tgg ttc aat ctc ata ttt aaa tgg ata ttg ttt ggc cat cgt

299

Gly Asp Trp Phe Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg
65 70 75

cct tac tgg tgg ata caa gaa act gag att tat cca aat cat tca agc

347

Pro Tyr Trp Trp Ile Gln Glu Thr Glu Ile Tyr Pro Asn His Ser Ser
80 85 90 95

cca tgt ctt gag cag ttt cct act acg tgt gaa aca ggc cca gga agt

395

Pro Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser
100 105 110

cca tct ggc cac gca atg ggc tca tcg tgc gtc tgg tat gtc atg gta

443

Pro Ser Gly His Ala Met Gly Ser Ser Cys Val Trp Tyr Val Met Val
115 120 125

aca gct gcc cta agc tac acc atc agc cgg atg gag gag tcc tct gtc

491

Thr Ala Ala Leu Ser Tyr Thr Ile Ser Arg Met Glu Glu Ser Ser Val
130 135 140

act ctg cac aga ctg acc tgg tcc ttt ctg tgg agt gtt ttc tgg ttg

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539
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 587
 Ile Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe
 160 165 170 175
 ccc cat cag gtc att ctt gga gtg att ggt ggg atg cta gta gcc gag
 635
 Pro His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu
 180 185 190
 gcc ttt gaa cac act cca gga gtc cac atg gcc agc ttg agt gtg tac
 683
 Ala Phe Glu His Thr Pro Gly Val His Met Ala Ser Leu Ser Val Tyr
 195 200 205
 ctg aag acc aac gtc ttc ctc ttc ctg ttt gcc ctc ggc ttt tac ctg
 731
 Leu Lys Thr Asn Val Phe Leu Phe Leu Phe Ala Leu Gly Phe Tyr Leu
 210 215 220
 ctt ctc cga ctg ttc ggt att gac ctg ctg tgg tcc gtg ccc atc gcc
 779
 Leu Leu Arg Leu Phe Gly Ile Asp Leu Leu Trp Ser Val Pro Ile Ala
 225 230 235
 aaa aag tgg tgt gcc aac cca gac tgg atc cac att gac agc acg cct
 827
 Lys Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Ser Thr Pro
 240 245 250 255
 ttt gct gga ctc gtg aga aac ctc ggg gtc ctc ttt ggc ttg ggt ttc
 875
 Phe Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe
 260 265 270
 gcc atc aac tca gaa atg ttc ctt cgg agc tgc cag gga gaa aat ggc
 923
 Ala Ile Asn Ser Glu Met Phe Leu Arg Ser Cys Gln Gly Glu Asn Gly
 275 280 285
 acc aag ccg agc ttc cgc ttg ctc tgt gct ctg acc tca ctg acc aca
 971
 Thr Lys Pro Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Thr
 290 295 300
 atg caa ctt tat cgc ttc atc aag atc ccg act cac gcg gaa cct tta
 1019
 Met Gln Leu Tyr Arg Phe Ile Lys Ile Pro Thr His Ala Glu Pro Leu
 305 310 315
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 20 25 30

Gly Asp Pro Arg Asn Ile Phe Ser Ile Tyr Phe Pro Leu Trp Phe Gln
 35 40 45

Leu Asn Gln Asn Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
 50 55 60

Asp Trp Phe Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
 65 70 75 80

Tyr Trp Trp Ile Gln Glu Thr Glu Ile Tyr Pro Asn His Ser Ser Pro
 85 90 95

Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
 100 105 110

Ser Gly His Ala Met Gly Ser Ser Cys Val Trp Tyr Val Met Val Thr
 115 120 125

Ala Ala Leu Ser Tyr Thr Ile Ser Arg Met Glu Glu Ser Ser Val Thr
 130 135 140

Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
 145 150 155 160

Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
 165 170 175

His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
 180 185 190

Phe Glu His Thr Pro Gly Val His Met Ala Ser Leu Ser Val Tyr Leu
 195 200 205

Lys Thr Asn Val Phe Leu Phe Leu Phe Ala Leu Gly Phe Tyr Leu Leu
 210 215 220

Leu Arg Leu Phe Gly Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
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Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Ser Thr Pro Phe
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2848-56-PCT.ST25.txt

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<212> PRT

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<223> artificial Mus sp.

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